

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/702,718

1649

DATE: 08/18/98  
TIME: 13:46:24

INPUT SET: S28089.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

- 1
- 2
- 3 (1) General Information:
- 4
- 5 (i) APPLICANT: Muller-Rober, Bernd
- 6 Land-Schutze, Volker
- 7 La Cognata, Ursula
- 8
- 9 (ii) TITLE OF INVENTION: PROCESSES FOR INHIBITING AND FOR
- 10 INDUCING FLOWER FORMATION IN PLANTS
- 11
- 12 (iii) NUMBER OF SEQUENCES: 14
- 13
- 14 (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: FISH & NEAVE
- 16 (B) STREET: 1251 Avenue of the Americas
- 17 (C) CITY: New York
- 18 (D) STATE: New York
- 19 (E) COUNTRY: USA
- 20 (F) ZIP: 10020
- 21
- 22 (v) COMPUTER READABLE FORM:
- 23 (A) MEDIUM TYPE: Floppy disk
- 24 (B) COMPUTER: IBM PC compatible
- 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 27
- 28 (vi) CURRENT APPLICATION DATA:
- 29 (A) APPLICATION NUMBER: US 08/702,718
- 30 (B) FILING DATE: 19-MAR-1997
- 31
- 32 (vii) PRIOR APPLICATION DATA:
- 33 (A) APPLICATION NUMBER: DE P4408629.6
- 34 (B) FILING DATE: 09-MAR-1994
- 35
- 36 (vii) PRIOR APPLICATION DATA:
- 37 (A) APPLICATION NUMBER: DE P4435366.9
- 38 (B) FILING DATE: 22-SEP-1994
- 39
- 40 (vii) PRIOR APPLICATION DATA:
- 41 (A) APPLICATION NUMBER: DE P4438821.7
- 42 (B) FILING DATE: 19-OCT-1994
- 43
- 44 (viii) ATTORNEY/AGENT INFORMATION:
- 45 (A) NAME: Haley Jr., James F.
- 46 (B) REGISTRATION NUMBER: 27,794

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/702,718DATE: 08/18/98  
TIME: 13:46:25

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47 (C) REFERENCE/DOCKET NUMBER: AGREVO-1  
48  
49 (ix) TELECOMMUNICATION INFORMATION:  
50 (A) TELEPHONE: 212-596-9000  
51 (B) TELEFAX: 212-596-9090  
52  
53  
54 (2) INFORMATION FOR SEQ ID NO:1:  
55  
56 (i) SEQUENCE CHARACTERISTICS:  
57 (A) LENGTH: 1891 base pairs  
58 (B) TYPE: nucleic acid  
59 (C) STRANDEDNESS: unknown  
60 (D) TOPOLOGY: linear  
61  
62 (ii) MOLECULE TYPE: cDNA to mRNA  
63  
64 (iii) HYPOTHETICAL: NO  
65  
66 (iv) ANTI-SENSE: NO  
67  
68 (vi) ORIGINAL SOURCE:  
69 (A) ORGANISM: Solanum tuberosum  
70 (B) STRAIN: c.v. Desiree  
71 (F) TISSUE TYPE: leaf  
72  
73 (vii) IMMEDIATE SOURCE:  
74 (A) LIBRARY: cDNA library in pBluescriptKS  
75 (B) CLONE: pCBS  
76  
77 (ix) FEATURE:  
78 (A) NAME/KEY: CDS  
79 (B) LOCATION: 73..1485  
80 (D) OTHER INFORMATION: /EC\_number= 4.1.3.7.  
81 /product= "Citrate synthase"  
82  
83  
84 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
85  
86 TTTTTCGTTC CATCAGCCTA CTTGAGATGT ATTCCCACTG GTAAAAGTTA ATTTTTTTTGA 60  
87  
88 TTTTCGCGAG CA ATG GTG TTC TAC CGT AGC GTT TCG TTG CTG TCA AAG 108  
89 Met Val Phe Tyr Arg Ser Val Ser Leu Ser Lys  
90 1 5 10  
91  
92 CTC CGC TCT CGA GCG GTC CAA CAG TCA AAT GTT AGC AAT TCT GTG CGC 156  
93 Leu Arg Ser Arg Ala Val Gln Gln Ser Asn Val Ser Asn Ser Val Arg  
94 15 20 25  
95  
96 TGG CTT CAA GTC CAA ACC TCT TCC GGT CTT GAT CTG CGT TCT GAG CTG 204  
97 Trp Leu Gln Val Gln Thr Ser Ser Gly Leu Asp Leu Arg Ser Glu Leu  
98 30 35 40  
99

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/702,718

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100	GTA CAA GAA TTG ATT CCT GAA CAA CAG GAT CGC CTG AAA AAG ATC AAG	252
101	Val Gln Glu Leu Ile Pro Glu Gln Gln Asp Arg Leu Lys Lys Ile Lys	
102	45 50 55 60	
103		
104	TCA GAT ATG AAA GGT TCA ATT GGG AAC ATC ACA GTT GAT ATG GTT CTT	300
105	Ser Asp Met Lys Gly Ser Ile Gly Asn Ile Thr Val Asp Met Val Leu	
106	65 70 75	
107		
108	GGT GGA ATG AGA GGA ATG ACA GGA TTA CTG TGG AAA CCT CAT TAC CTT	348
109	Gly Gly Met Arg Gly Met Thr Gly Leu Trp Lys Pro His Tyr Leu	
110	80 85 90	
111		
112	GAC CCT GAT GAG GGA ATT CGC TTC CGG GGG TTG TCT ATA CCT GAA TGC	396
113	Asp Pro Asp Glu Gly Ile Arg Phe Arg Gly Leu Ser Ile Pro Glu Cys	
114	95 100 105	
115		
116	CAA AAG GTA TTA CCT GCA GCA AAG CCT GGG GGT GAG CCC TTG CCT GAA	444
117	Gln Lys Val Leu Pro Ala Ala Lys Pro Gly Gly Glu Pro Leu Pro Glu	
118	110 115 120	
119		
120	GGT CTT CTC TGG CTT CTT TTA ACA GGA AAG GTG CCA TCA AAA GAG CAA	492
121	Gly Leu Leu Trp Leu Leu Leu Thr Gly Lys Val Pro Ser Lys Glu Gln	
122	125 130 135 140	
123		
124	GTG AAT TCA ATT GTC TCA GGA ATT GCA GAG TCG GGC ATC ATA TCC CTG	540
125	Val Asn Ser Ile Val Ser Gly Ile Ala Glu Ser Gly Ile Ile Ser Leu	
126	145 150 155	
127		
128	ATC ATC ATG TAT ACA ACT ATT GAT GCC TTA CCA GTC ACA GCT CAT CCA	588
129	Ile Ile Met Tyr Thr Thr Ile Asp Ala Leu Pro Val Thr Ala His Pro	
130	160 165 170	
131		
132	ATG ACC CAG TTT GCT ACT GGA GTC ATG GCT CTT CAG GTT CAA AGT GAA	636
133	Met Thr Gln Phe Ala Thr Gly Val Met Ala Leu Gln Val Gln Ser Glu	
134	175 180 185	
135		
136	TTT CAA AAG GCA TAC GAG AAA GGG ATT CAC AAA TCA AAG TAT TGG GAA	684
137	Phe Gln Lys Ala Tyr Glu Lys Gly Ile His Lys Ser Lys Tyr Trp Glu	
138	190 195 200	
139		
140	CCA ACA TAT GAG GAT TCC ATG AAT CTG ATT GCT CAA GTT CCA CTT GTT	732
141	Pro Thr Tyr Glu Asp Ser Met Asn Leu Ile Ala Gln Val Pro Leu Val	
142	205 210 215 220	
143		
144	GCT GCT TAT GTT TAT CGC AGG ATG TAC AAG AAT GGT GAC ACT ATA CCT	780
145	Ala Ala Tyr Val Tyr Arg Arg Met Tyr Lys Asn Gly Asp Thr Ile Pro	
146	225 230 235	
147		
148	AAG GAT GAA TCC CTG GAT TAT GGT GCA AAT TTT GCT CAC ATG CTT GGT	828
149	Lys Asp Glu Ser Leu Asp Tyr Gly Ala Asn Phe Ala His Met Leu Gly	
150	240 245 250	
151		
152	TTC AGT AGC TCT GAA ATG CAT GAA CTT CTT ATG AGG CTC TAT GTA ACA	876

# RAW SEQUENCE LISTING PATENT APPLICATION *US/08/702,718*

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153	Phe	Ser	Ser	Ser	Glu	Met	His	Glu	Leu	Leu	Met	Arg	Leu	Tyr	Val	Thr	
154			255					260					265				
155																	
156	ATA	CAC	AGT	GAT	CAT	GAA	GGT	GGT	AAT	GTC	AGT	GCT	CAC	ACC	GGT	CAC	924
157	Ile	His	Ser	Asp	His	Glu	Gly	Gly	Asn	Val	Ser	Ala	His	Thr	Gly	His	
158		270					275					280					
159																	
160	TTG	GTT	GCT	AGT	GCT	TTG	TCT	GAT	CCT	TAC	CTC	TCC	TTT	GCT	GCT	GCT	972
161	Leu	Val	Ala	Ser	Ala	Leu	Ser	Asp	Pro	Tyr	Leu	Ser	Phe	Ala	Ala	Ala	
162	285					290					295					300	
163																	
164	TTG	AAT	GGT	TTA	GCC	GGA	CCA	CTT	CAT	GGT	TTA	GCC	AAT	CAG	GAA	GTT	1020
165	Leu	Asn	Gly	Leu	Ala	Gly	Pro	Leu	His	Gly	Leu	Ala	Asn	Gln	Glu	Val	
166					305					310					315		
167																	
168	TTG	CTA	TGG	ATA	AAA	TCT	GTT	GTA	GAA	GAA	TGT	GGG	GAG	AAC	ATT	TCC	1068
169	Leu	Leu	Trp	Ile	Lys	Ser	Val	Val	Glu	Glu	Cys	Gly	Glu	Asn	Ile	Ser	
170				320					325				330				
171																	
172	AAA	GAG	CAG	TTG	AAA	GAC	TAT	GTT	TGG	AAA	ACA	TTG	AAC	AGT	GGC	AAG	1116
173	Lys	Glu	Gln	Leu	Lys	Asp	Tyr	Val	Trp	Lys	Thr	Leu	Asn	Ser	Gly	Lys	
174			335					340					345				
175																	
176	GTT	GTC	CCT	GGT	TTT	GGA	CAT	GGA	GTT	CTG	CGA	AAG	ACT	GTA	CCA	AGA	1164
177	Val	Val	Pro	Gly	Phe	Gly	His	Gly	Val	Leu	Arg	Lys	Thr	Val	Pro	Arg	
178		350					355					360					
179																	
180	TAT	ACA	TGC	CAG	AGA	GAG	TTC	GCT	ATG	AAG	CAT	TTG	CCT	GAA	GAT	CCA	1212
181	Tyr	Thr	Cys	Gln	Arg	Glu	Phe	Ala	Met	Lys	His	Leu	Pro	Glu	Asp	Pro	
182	365					370					375					380	
183																	
184	CTG	TTT	CAA	CTG	GTT	TCA	AAA	CTC	TAC	GAA	GTT	TTC	CTC	CTG	TTC	TTA	1260
185	Leu	Phe	Gln	Leu	Val	Ser	Lys	Leu	Tyr	Glu	Val	Phe	Leu	Leu	Phe	Leu	
186					385					390					395		
187																	
188	CAG	AAC	TTG	GCA	AAG	TTA	AAA	CCT	TGG	CCA	AAT	GTT	GAT	GCC	CAC	AGT	1308
189	Gln	Asn	Leu	Ala	Lys	Leu	Lys	Pro	Trp	Pro	Asn	Val	Asp	Ala	His	Ser	
190				400					405					410			
191																	
192	GGT	GTG	TTG	TTG	AAC	TAT	TAT	GGT	TTA	ACT	GAA	GCA	AGA	TAT	TAT	ACG	1356
193	Gly	Val	Leu	Leu	Asn	Tyr	Tyr	Gly	Leu	Thr	Glu	Ala	Arg	Tyr	Tyr	Thr	
194			415					420					425				
195																	
196	GTC	CTC	TTT	GGC	GTA	TCA	AGA	GCT	CTT	GGC	ATT	TGC	TCT	CAG	CTA	ATT	1404
197	Val	Leu	Phe	Gly	Val	Ser	Arg	Ala	Leu	Gly	Ile	Cys	Ser	Gln	Leu	Ile	
198		430					435					440					
199																	
200	TGG	GAC	CGA	GCT	CTT	GGA	TTG	CCG	CTA	GAG	AGG	CCA	AAG	AGT	GTC	ACA	1452
201	Trp	Asp	Arg	Ala	Leu	Gly	Leu	Pro	Leu	Glu	Arg	Pro	Lys	Ser	Val	Thr	
202	445					450					455					460	
203																	
204	ATG	GAG	TGG	CTT	GAG	AAC	CAG	TGC	AAG	AAA	GCA	TGAATTGTTT	GAAATCTCGC				1505
205	Met	Glu	Trp	Leu	Glu	Asn	Gln	Cys	Lys	Lys	Ala						

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206          465          470
207
208 GAGCATAAAA CACAATGTAT AATCTCTATG AATAATTGCT TGACAAAGCA CTCCTTTCTT 1565
209
210 GGGGGACAAG ATAGGTCGGC CCTTCAATGG GTTAACGAAC TTCAGTTCAA ACTTCACTGA 1625
211
212 ATTTGTGTGA ATTGTATGGT TTCTCGAGAC TTGTCCTGAA TTTTGAACCTT AGTCTAGTGG 1685
213
214 ATTCATTTTT CTTCATTCCG AATTCCTCAC ACGCTGATCC AGCATGTAAA AATTAATAGG 1745
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216 TCAATGCTAT TAATCGCGTT CTTGGTTGCC ATTAGACTTG TGAATGACTT CCTTTGCTGG 1805
217
218 AAAGTTAGTA ATCGGCTGAT TCACGCAATA AACTGCAATT GTGTAGTTTC TTAAATTTGC 1865
219
220 TAATTCTTAT TTGATGATAT TATGAA 1891
221
222

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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233
234 Met Val Phe Tyr Arg Ser Val Ser Leu Leu Ser Lys Leu Arg Ser Arg
235   1             5             10             15
236
237 Ala Val Gln Gln Ser Asn Val Ser Asn Ser Val Arg Trp Leu Gln Val
238   20             25             30
239
240 Gln Thr Ser Ser Gly Leu Asp Leu Arg Ser Glu Leu Val Gln Glu Leu
241   35             40             45
242
243 Ile Pro Glu Gln Gln Asp Arg Leu Lys Lys Ile Lys Ser Asp Met Lys
244   50             55             60
245
246 Gly Ser Ile Gly Asn Ile Thr Val Asp Met Val Leu Gly Gly Met Arg
247   65             70             75             80
248
249 Gly Met Thr Gly Leu Leu Trp Lys Pro His Tyr Leu Asp Pro Asp Glu
250   85             90             95
251
252 Gly Ile Arg Phe Arg Gly Leu Ser Ile Pro Glu Cys Gln Lys Val Leu
253   100            105            110
254
255 Pro Ala Ala Lys Pro Gly Gly Glu Pro Leu Pro Glu Gly Leu Leu Trp
256   115            120            125
257
258 Leu Leu Leu Thr Gly Lys Val Pro Ser Lys Glu Gln Val Asn Ser Ile

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PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/702,718**

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Line

Error

Original Text